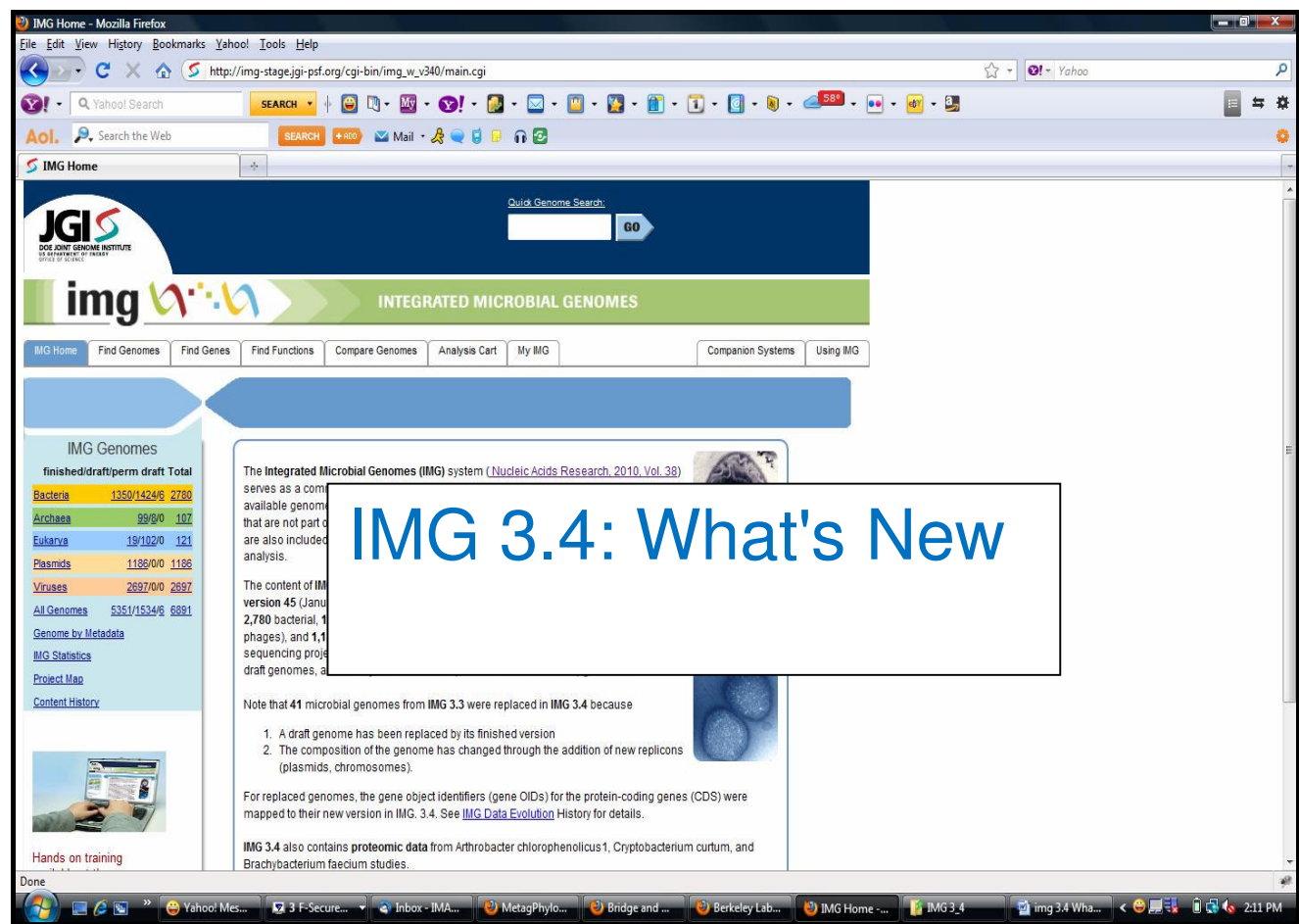


What's New in IMG 3.4



The screenshot shows the IMG 3.4 homepage in a Mozilla Firefox browser. The page has a blue header with the JGI logo and a search bar. Below the header is a green banner with the text "img INTEGRATED MICROBIAL GENOMES". A navigation menu includes links for "IMG Home", "Find Genomes", "Find Genes", "Find Functions", "Compare Genomes", "Analysis Cart", "My IMG", "Companion Systems", and "Using IMG".

On the left side, there is a section titled "IMG Genomes" with a table showing the number of finished, draft, and permanent genomes for various organisms. Below the table are links for "Genome by Metadata", "IMG Statistics", "Project Map", and "Content History".

The main content area features a large blue box with the text "IMG 3.4: What's New". To the right of this box, there is a section titled "The Integrated Microbial Genomes (IMG) system" with a link to "Nucleic Acids Research, 2010, Vol. 38". Below this, there is a section titled "The content of IMG version 45" with a link to "Janu 2, 2010".

Below the main content area, there is a section titled "Note that 41 microbial genomes from IMG 3.3 were replaced in IMG 3.4 because" with a list of reasons:

1. A draft genome has been replaced by its finished version
2. The composition of the genome has changed through the addition of new replicons (plasmids, chromosomes).

Below the list, there is a section titled "For replaced genomes, the gene object identifiers (gene OIDs) for the protein-coding genes (CDS) were mapped to their new version in IMG. 3.4. See [IMG Data Evolution History](#) for details."

At the bottom of the page, there is a section titled "IMG 3.4 also contains proteomic data from Arthrobacter chlorophenolicus 1, Cryptobacterium curtum, and Brachyobacterium faecium studies."

The browser's address bar shows the URL "http://img-stage.jgi-psf.org/cgi-bin/img_w_v340/main.cgi". The browser's status bar shows the time "2:11 PM".

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IMG 3.4 Content Genomes

The content of **IMG 3.4** has been updated with new microbial genomes available in **RefSeq version 45** (January 14, 2011). **IMG 3.4** contains a total of **6,423** genomes consisting of **2,780** bacterial, **107** archaeal, **121** eukaryotic genomes, **2,697** viruses (including bacterial phages), and **1,186** plasmids that did not come from a specific microbial genome sequencing project. Among these genomes, **5,351** are **finished** genomes, and **1,540** are **draft** genomes, and **4** are **permanent draft** (i.e., will never be finished) genomes.

Note that **41** microbial genomes from **IMG 3.3** were **replaced** in **IMG 3.4** because (1) a **draft** genome has been replaced by its **finished** version, or (2) the composition of the genome has changed through the addition of new replicons (plasmids, chromosomes). For replaced genomes, the gene object identifiers (gene OIDs) for the protein-coding genes (CDS) were mapped to their new version in **IMG 3.4**. See IMG Data Evolution History for details.

IMG 3.4 also contains **proteomic** data from *Arthrobacter chlorophenolicus*1, *Cryptobacterium curtum*, and *Brachybacterium faecium* studies.

IMG Statistics

Various statistics are provided via the **IMG Statistics** link on the home page of IMG, as shown below, including **IMG Total Gene Count** which consists of counting all the genes (protein coding genes, RNA genes) in IMG, except obsolete genes. Compared to **IMG 3.3**, **IMG 3.4** contains **11,634,737 genes**, an increase of **1,483,215 genes**.

The following (45) eukaryotic genomes have been included into IMG in order to increase its genomic context for comparative analysis. Currently there are **121 Eukaryotic genomes in IMG 3.4**.

IMG 3.4 (July 2011) – 45 Genomes

Fungal Genomes

1. *Ajellomyces dermatitidis* SLH14081
2. *Arthroderma benhamiae* CBS 112371
3. *Arthroderma gypseum* CBS 118893
4. *Arthroderma otae* CBS 113480
5. *Clavospora lusitaniae* ATCC 42720
6. *Coccidioides posadasii* C735 delta SOWgp
7. *Nectria haematococca* mpVI 77-13-4 ([JGI](#))
8. *Paracoccidioides brasiliensis* Pb01
9. *Schizophyllum commune* H4-8 ([JGI](#))
10. *Trichophyton verrucosum* HKI 0517
11. *Tuber melanosporum* Mel28
12. *Uncinocarpus reesii* 1704
13. *Verticillium albo-atrum* VaMs.102

What's New in IMG 3.4

Plants

1. *Arabidopsis lyrata* subsp. *Lyrata* (JGI)
2. *Chlamydomonas reinhardtii* (JGI)
3. *Micromonas pusilla* CCMP1545 (JGI)
4. *Physcomitrella patens* subsp. *Patens* (JGI)
5. *Populus trichocarpa* (JGI)
6. *Ricinus communis*
7. *Sorghum bicolor*
8. *Vitis vinifera*

Insects

1. *Acyrtosiphon pisum*
2. *Aedes aegypti*
3. *Apis mellifera*
4. *Culex quinquefasciatus*
5. *Drosophila ananassae*
6. *Drosophila erecta*
7. *Drosophila grimshawi*
8. *Drosophila mojavensis*
9. *Drosophila persimilis*
10. *Drosophila pseudoobscura pseudoobscura*
11. *Drosophila sechellia*
12. *Drosophila virilis*
13. *Drosophila willistoni*
14. *Drosophila yakuba*
15. *Nasonia vitripennis*
16. *Pediculus humanus corporis*
17. *Tribolium castaneum*

Protists

1. *Babesia bovis* T2Bo
2. *Monosiga brevicollis* MX1 (JGI)
3. *Naegleria gruberi* strain NEG-M (JGI)
4. *Nosema ceranae* BRL01
5. *Perkinsus marinus* ATCC 50983
6. *Phaeodactylum tricornutum* CCAP 1055/1 (JGI)
7. *Thalassiosira pseudonana* CCMP1335 (JGI)

IMG 3.4 UI

New UI Features

Radial Phylogenetic Tree

Users have the ability to view up to five genomes phylogenetically in a circular tree. This new tool is found under menu “Compare Genomes” - Phylogenetic Tree, see Figure 1. Hovering mouse over tree will display popup window of detail information of the node.

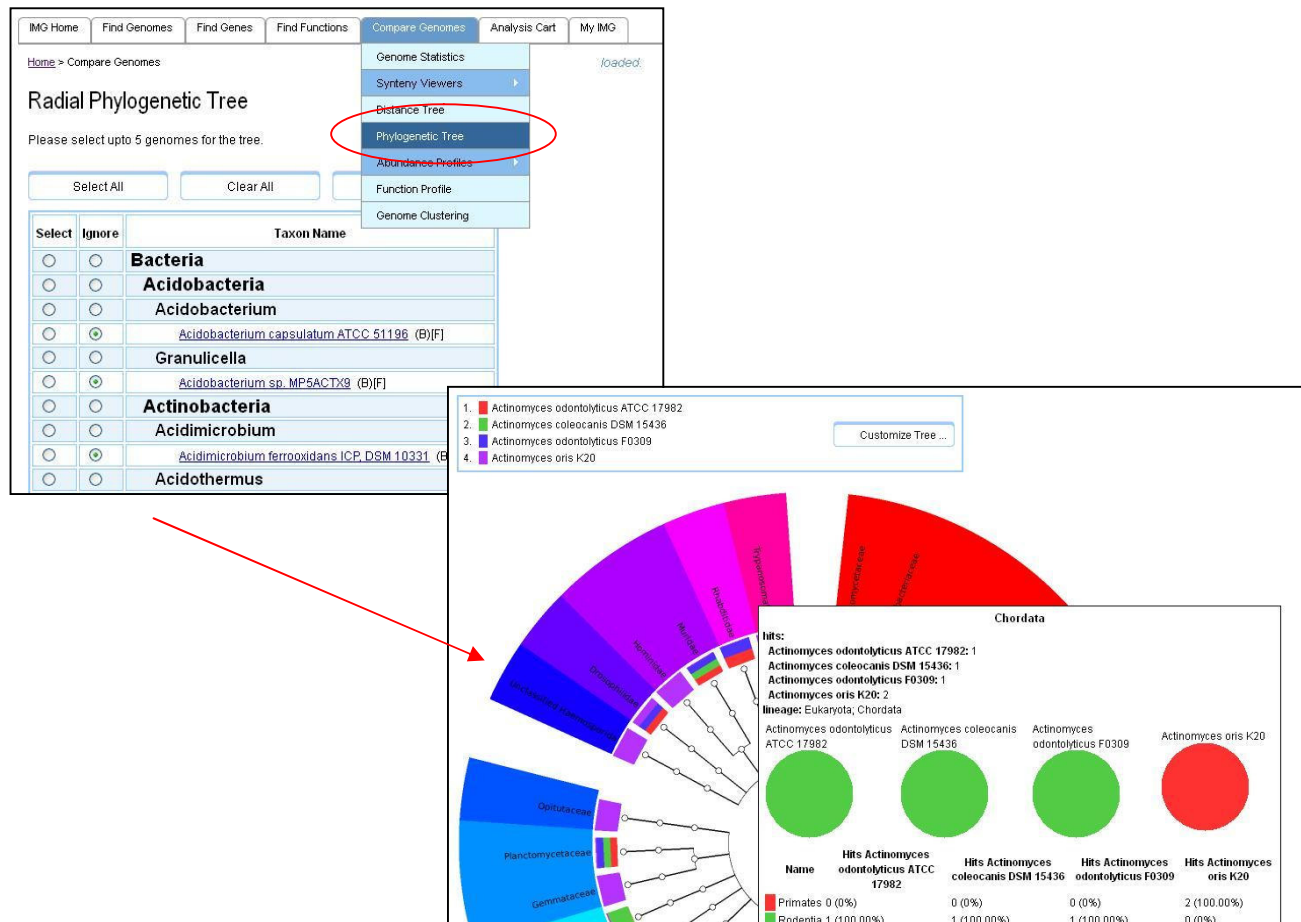


Figure 1 Phylogenetic Tree

Tree display can be customized by click “Customize Tree” button, see Figure 2.

- Taxonomic rank / tree level by: Domain, Phylum/Class, Order and Family
- Color group by: Domain, Phylum/Class, Order and Family
- Genome sample weight graph: Stacked, Bar
- Resize tree: Title space and Diameter

What's New in IMG 3.4

Tree

Current view of the tree is rendered by **family** and colored by **phylum**. To change these settings, click on the *Customize Tree* button.

1. ■ Sulfolobus acidocaldarius DSM 639
2. ■ Sulfolobus islandicus L.S.2.15
3. ■ Sulfolobus islandicus L.D.8.5
4. ■ Sulfolobus islandicus HVE10/4

Customize Tree ...

Customize Tree

Parameter	Setting
Taxonomic rank to view by	Family
Color groups by	Phylum/Class
Genome sample weight graph	Stacked
Title space width (150-600)	300 px
Diameter of the tree (600-1500)	800 px

Redraw

Cancel

Figure 2 Customize phylogenetic tree display

Genome Cart

Users now have the ability to add and remove individual genomes to their cart. As before user can selected their genomes in Genome Browser. Instead of saving and replacing genomes, you now can add addition genomes to your genome cart. The genome cart is found under menu “Analysis Cart” – Genomes, see Figure 3.

What's New in IMG 3.4

Genome Browser

hint: Go to [Preferences](#) to show or hide plasmids and viruses.
Go to home page statistics under [IMG Genomes](#) to select individual phylogenetic domains or all genomes.

Domains(D): B=Bacteria, A=Archaea, E=Eukarya, P=Plasmids, V=Viruses.
Genome Completion(C): F=Finished, P=Permanent Draft, D=Draft.

[Add Selected to Genome Cart](#) [Select All](#) [Clear All](#) [View Phylogenetical](#)

Filter column: [Domain](#) Filter term:

[Export](#) Page 1 of 31 << first < prev 1 2 3 4 5 6 7 8 9 10 next > last >> 100

Column Selector [Select Page](#) [Deselect Page](#)

Select	Domain	Status	Proposal Name	Genome
<input type="checkbox"/>	A	F	-	Acidilobus saccharovorans 345-15

Genome Cart

[Genome List](#) [Upload](#)

Genome List

100 genome(s) in cart

hint: View Genome's [Metadata](#) [Genome Metadata](#).
To add more genomes to cart, please use the [Genome Browser](#).

[Remove Selected](#) [Select All](#) [Clear All](#) [Toggle Selected](#)

Filter column: [Domain](#) Filter term:

[Export](#) Page 1 of 1 << first < prev 1 next > last >> 100

Column Selector [Select Page](#) [Deselect Page](#)

Select	Domain	Status	Genome Name	Sequencing Center	Gene Count
<input type="checkbox"/>	B	F	'Nostoc azollae' 0708	DOE Joint Genome Institute	5379
<input type="checkbox"/>	B	D	Abiotrophia defectiva ATCC 49176	Washington Univ	3342
<input type="checkbox"/>	B	F	Acarvochloris marina MBIC11017	Arizona State Univ, TGen, Washington Univ	8498

Figure 3 Genome Cart

KOG

New function KOG has been add to IMG

- User can browser or list KOG functions. KOG function is found under menu “Find Function” – KOG with sub menus KOG Browser and KOG List, see Figure 4. KOG Browser was group via KOG categories similar to COG categories. KOG UI features was modeled similar to COG. Thus, clicking any KOG category will give a list of KOG ID with genome counts.
- KOG gene count has been to Genome Detail pages, see Figure 5. Clicking gene count will display a table and pie chart of genes grouped by KOG categories.

What's New in IMG 3.4

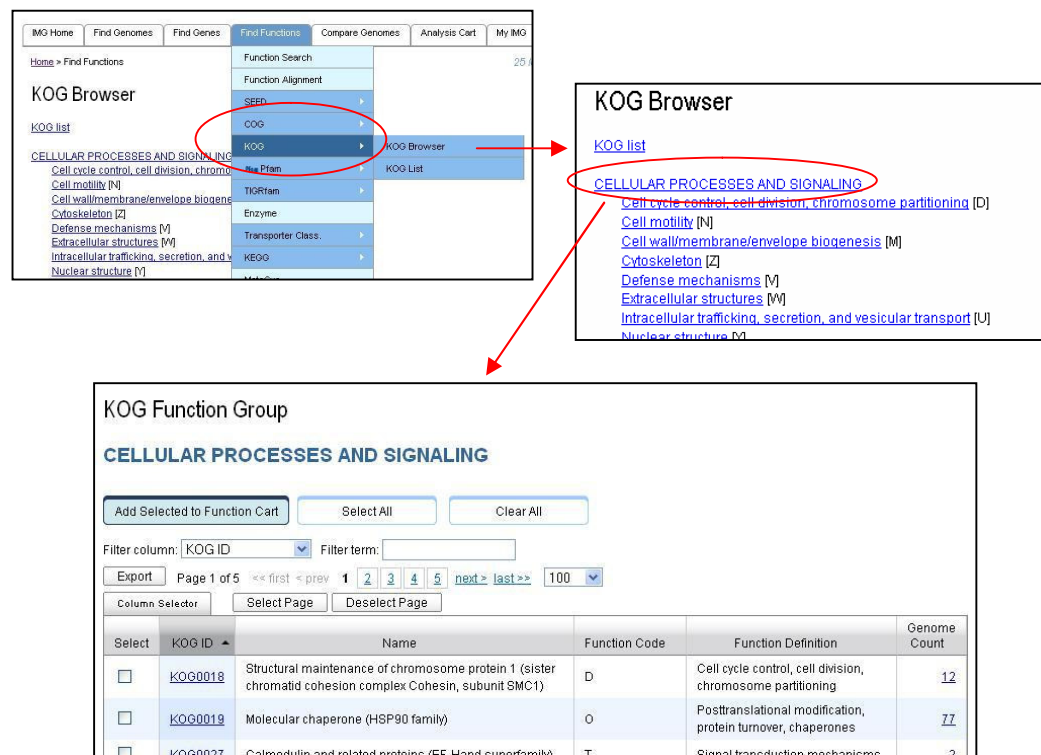


Figure 4 KOG Browser

Protein coding genes with COGs ³	1186	73.47%
with KOGs ³	828	69.57%
with Pfam ³	1186	75.36%
with TIGRfam ³	482	30.37%
with InterPro	1224	81.54%

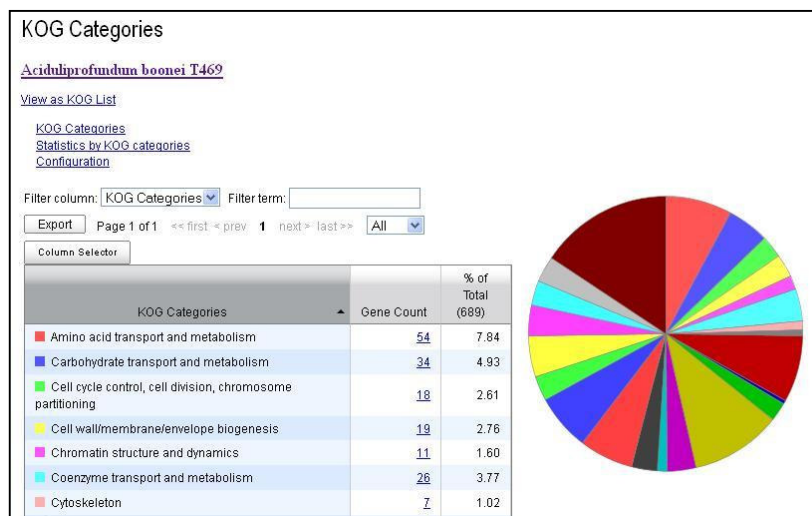


Figure 5 A genome's KOG gene list.

Updated UI Features

Genome Detail Page

Content list area has been reorganized. First there are three buttons on the top, see Figure 6

1. Browse Genome – A short cut to Browse Genome section.
2. BLAST Genome – A short cut to BLAST form with current genome pre-selected.
3. Download Data – A short cut to Genome's detail page download section or to the JGI Portal's download UI if the IMG's genome is available in Portal.

Content list renamed to "About Genome" and simplified to three sections, see Figure 7

1. Overview - A short cut to Overview section.
2. Statistics - A short cut to Statistics section.
3. Genes - A short cut to Gene section.

Abiotrophia defectiva ATCC 49176

[Browse Genome](#) [BLAST Genome](#) [Download Data](#)

About Genome

- Overview
- Statistics
- Genes

Overview

Proposal Name	Human Microbiome Project (HMP) Reference Genomes
Organism Name	Abiotrophia defectiva ATCC 49176
Taxon Object ID	643886181
NCBI Taxon ID	592010
RefSeq Project ID	56720

Download Selected Files ExpandAll CollapseAll

All Downloads

Additional Files

- Abide_643886181: [643886181.tar.gz](#)

Credits Disclaimer Comments/Questions

© 1997-2011 The Regents of the University of California.
Genome Portal version: 6.0.97.12500 content: 6.0.97.12501 clustering: >3118 synteny: no syn

Browse Genome

Scaffolds and Contigs

Chromosome Maps

Web Artemis

Phylogenetic Distribution of Genes

Distribution by BLAST percent identities

Putative Horizontally Transferred Genes

Putative Horizontally Transferred

BLAST

Find matches in selected genomes ("All IMG genomes" if none are selected).
If there are genomes in your Genome Cart, please use "Show All/Selected Genomes" buttons.

Sequence

Program: [blastp \(Protein vs. Protein\)](#)

E-value: [1e-5](#)

Genome Filter

Domains: (B)acteria, (A)rchaea, (E)ukarya, (P)lasmiids, (V)iruses.
Genome Completion: (F)inished, (P)ermanent Draft, (D)raft.

Seq. Status: [All Finished](#), [Permanent Draft and Draft](#) Domain: [All](#)

[List](#) [Tree](#)

- Vulcanisaeta moulisovskia 768-28 (A)[F]
- Nostoc azollae 0708 (B)[F]
- Abiotrophia defectiva ATCC 49176 (B)[D]
- Acaryochloris marina MBIC11017 (B)[F]

Figure 6 Genome detail page content list re-organized, top three buttons.

What's New in IMG 3.4

About Genome

- Overview
- Statistics
- Genes

Overview

Proposal Name	Human Microbiome Project (HMP) Reference Genomes
Organism Name	Abiotrophia defectiva ATCC 49176
Taxon Object ID	643886181
NCBI Taxon ID	592010
RefSeq Project ID	55729

Overview

Proposal Name	Human Microbiome Project (HMP) Reference Genomes
Organism Name	Abiotrophia defectiva ATCC 49176
Taxon Object ID	643886181
NCBI Taxon ID	592010
RefSeq Project ID	55729
GenBank Project ID	33011
GOLD ID in IMG Database	Project Id: Gi03551
External Links	JGI Portal
Genome Type	isolate
Lineage	Bacteria; Firmicutes; Clostridia
Sequencing Status	Draft
IMG Release	IMGV 2.9
Comment	strain mixup -16S rRNA is ~10
Project Information	
GOLD ID	Gi03551

Phylogenetic Distribution of Genes

Distribution by BLAST percent identities

Putative Horizontally Transferred Genes

Putative Horizontally Transferred

Compare Gene Annotations

Compare Gene Annotations

Gene annotation values are precomputed and stored in a tab delimited file also viewable in Excel.

Genome Statistics

hint: To view rows that are zero, go to [MyIMG preferences](#) and set "Hide Zeroes in Genome Statistics" to "No".

	Number	% of Total
DNA, total number of bases	3477404	100.00%
DNA coding number of bases	3125495	89.88%
DNA G+C number of bases	1291495	37.14% ¹
DNA scaffolds	28	100.00%
CRISPR Count	1	
Genes total number	3342	100.00%
Protein coding genes	3291	98.47%
RNA genes	51	1.53%

Figure 7 Genome detail page content list re-organized, content list.

Gene Cart

Circular Map tool number of band selection has increased from 4 to 8, as request by many users, see Figure 8

Chromosome Map

Filter column: Gene Object ID Filter term:

Export

Column Selector

Gene Object ID	Locus Tag	Product Name	Start	End	Strand	Scaffold	Batch	Band 1	Band 2	Band 3	Band 4	Band 5	Band 6	Band 7	Band 8
646648043	Abou_0004	agmatinase (EC 3.5.3.11) (IMGterm)	2602	3474	+	Aciduliprofundum boonei T469 chromosome	1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
646648080	Abou_0039	carbamate kinase (EC:2.7.2.2)	42007	42936	-	Aciduliprofundum boonei T469 chromosome	1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
646648103	Abou_0061	serine hydroxymethyltransferase (EC 2.1.2.1) (IMGterm)	60703	62004	-	Aciduliprofundum boonei T469 chromosome	1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
646648126	Abou_0084	sulfide dehydrogenase (flavoprotein) subunit SufA (EC 1.8.1.-) (IMGterm)	82460	83890	-	Aciduliprofundum boonei T469 chromosome	1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Export

Figure 8 Gene cart circular map tool

CSS Menu

CSS menu has been update to be compatible with FireFox5.x and IE 8. In addition CSS menuis accessibility compatible too, text zoom and view zoom will scale correctly. As mention earlier CSS will not work for older IE's 6 or 7. For IE 8 users please **turn off compatibility** view as CSS menu will not work in IE 8's compatibility mode.

1. Find Functions. Sub-menus were added to quickly access function's sub-pages. For example KEGG has five sub pages.
2. Download menu added FTP policy and Data Usage Policy.

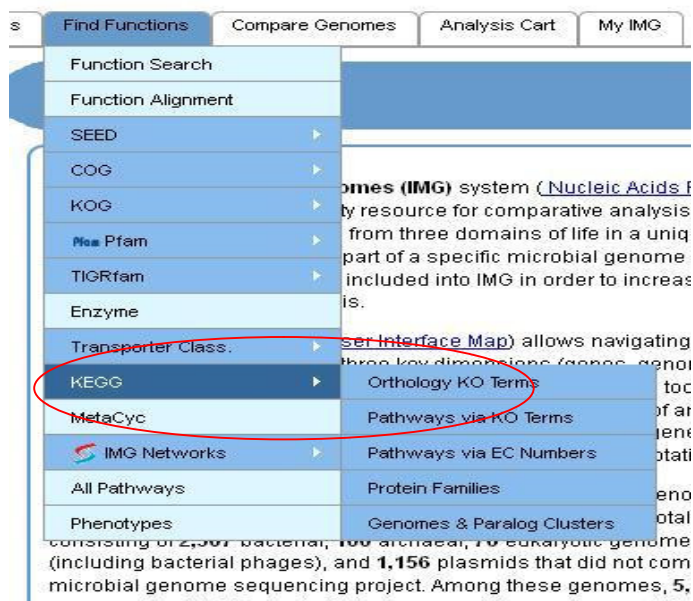


Figure 9 Function's sub pages were added as sub-menu for quicker access. For example KEGG function page has five sub pages.

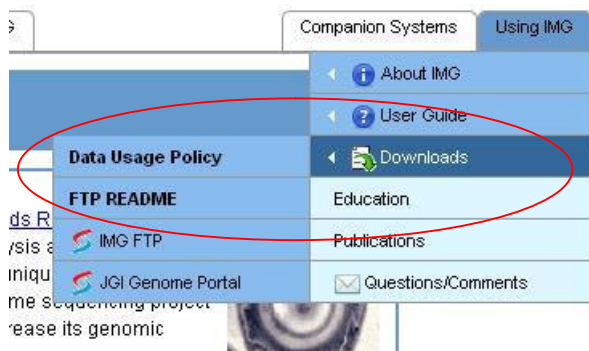


Figure 10 Two new sub-menus were added to download section: Data Usage Policy and FTP README.

Message Area

Message area was updated with additional warning messages.

What's New in IMG 3.4

1. Warning message for IE 6 to 7 users. IMG is no longer supporting older browsers because of IMG is using the latest JavaScript and CSS libraries.
2. Message area is being updated via AJAX. And will warn users of Browser and JavaScript support.
3. Users will also be informed for any IMG maintenance or downtime in this area too.

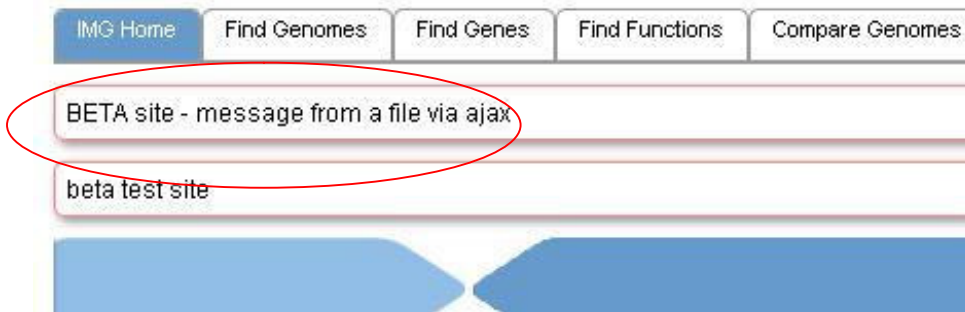


Figure 11 IMG's message area,

Google Maps

IMG's project map has been updated to use Google maps API version 3.x with clustering of Google push pins at higher zoom-out levels. Clicking clusters will zoom-in into the area, see Figure 12.

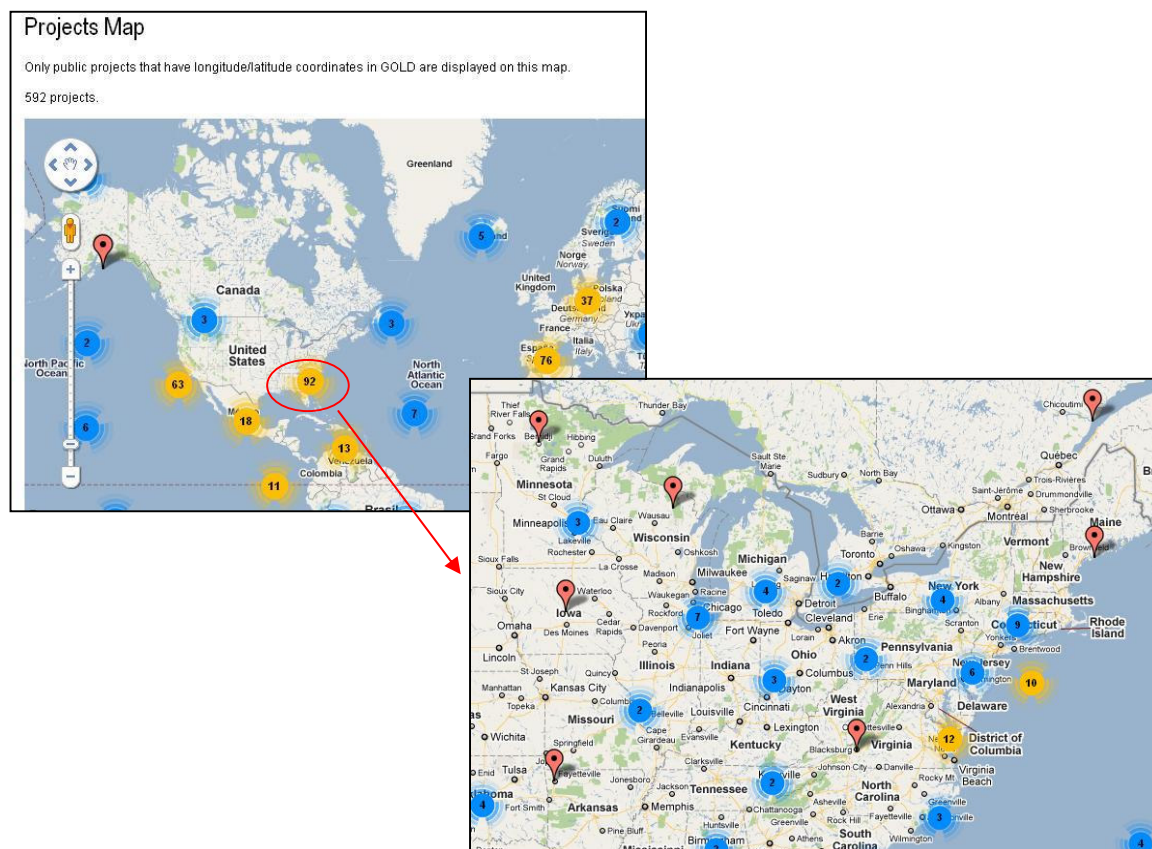


Figure 12 IMG's project map using Google push pin clustering.

Preferences

User can turn off session caching. It is recommended to leave it on for better UI performance.

Preferences

Parameter	Current Setting
Max. Paralog Groups	500 ▾
Max. Gene List Results	1000 ▾
Max. Homolog Results	200 ▾
Max. Taxon Gene Neighborhoods	15 ▾
Min. Homolog Percent Identity	30 ▾
Hide Viruses From Genome Lists	Yes ▾
Hide Plasmids From Genome Lists	Yes ▾
Hide Zeroes in Genome Statistics	Yes ▾
Session Cache On (Yes recommended)	Yes ▾

Figure 13 MyImg's preferences.

Phylogenetic Distance Tree

The [Archaeopterix applet](#) source code has been updated in IMG 3.4. The newest version of forester.jar has been merged with changes required for IMG. Additional changes are described below.

Use of system clipboard

In the current version of the applet, it is possible to copy from the "View as Text" window to the system clipboard and thus analyze the input file in various formats.

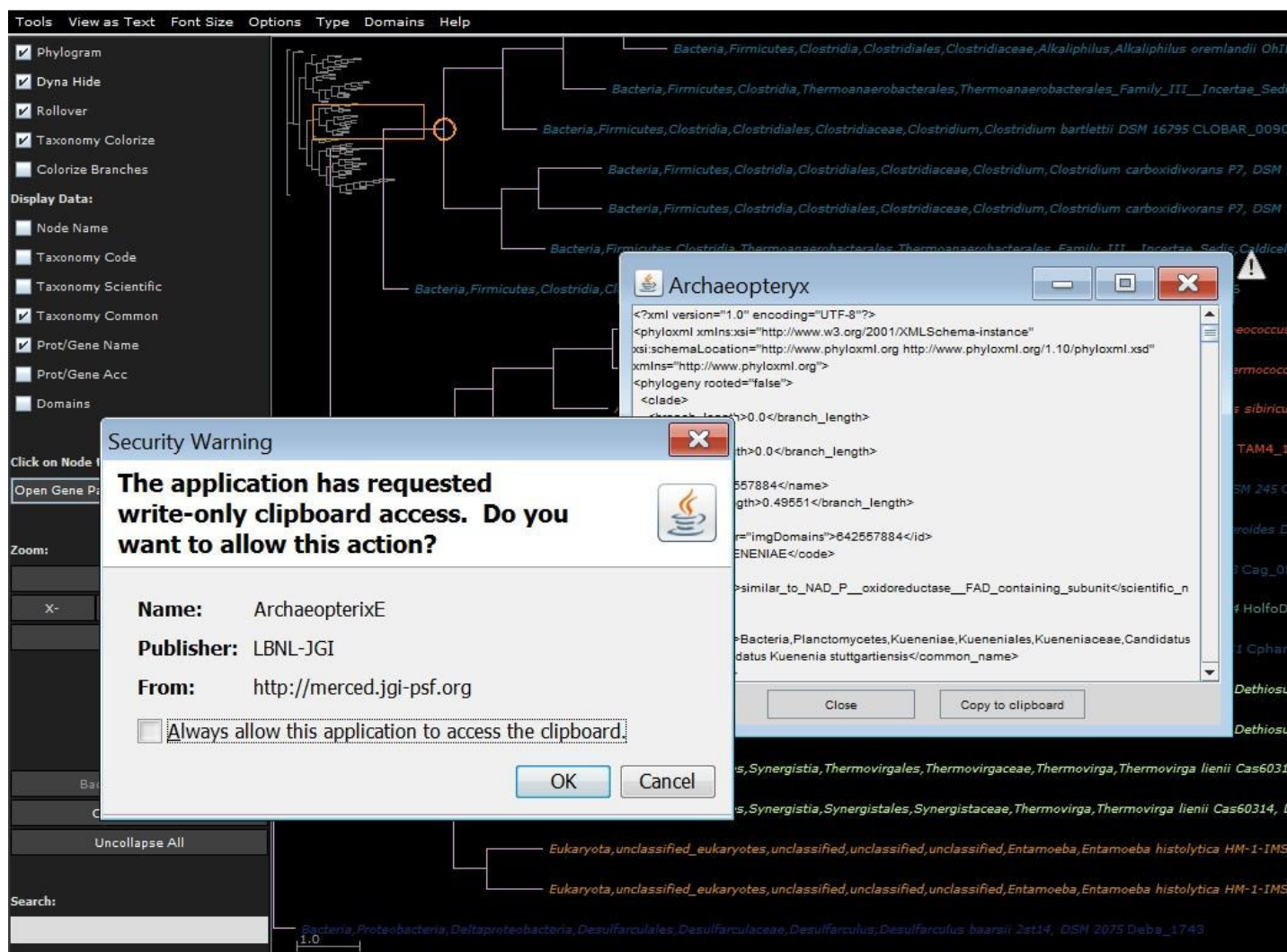


Figure 14 System clipboard

Lineage display

In the current version of the applet, the user can display the lineage of the node, and the common lineage of the parent nodes (in tooltip).

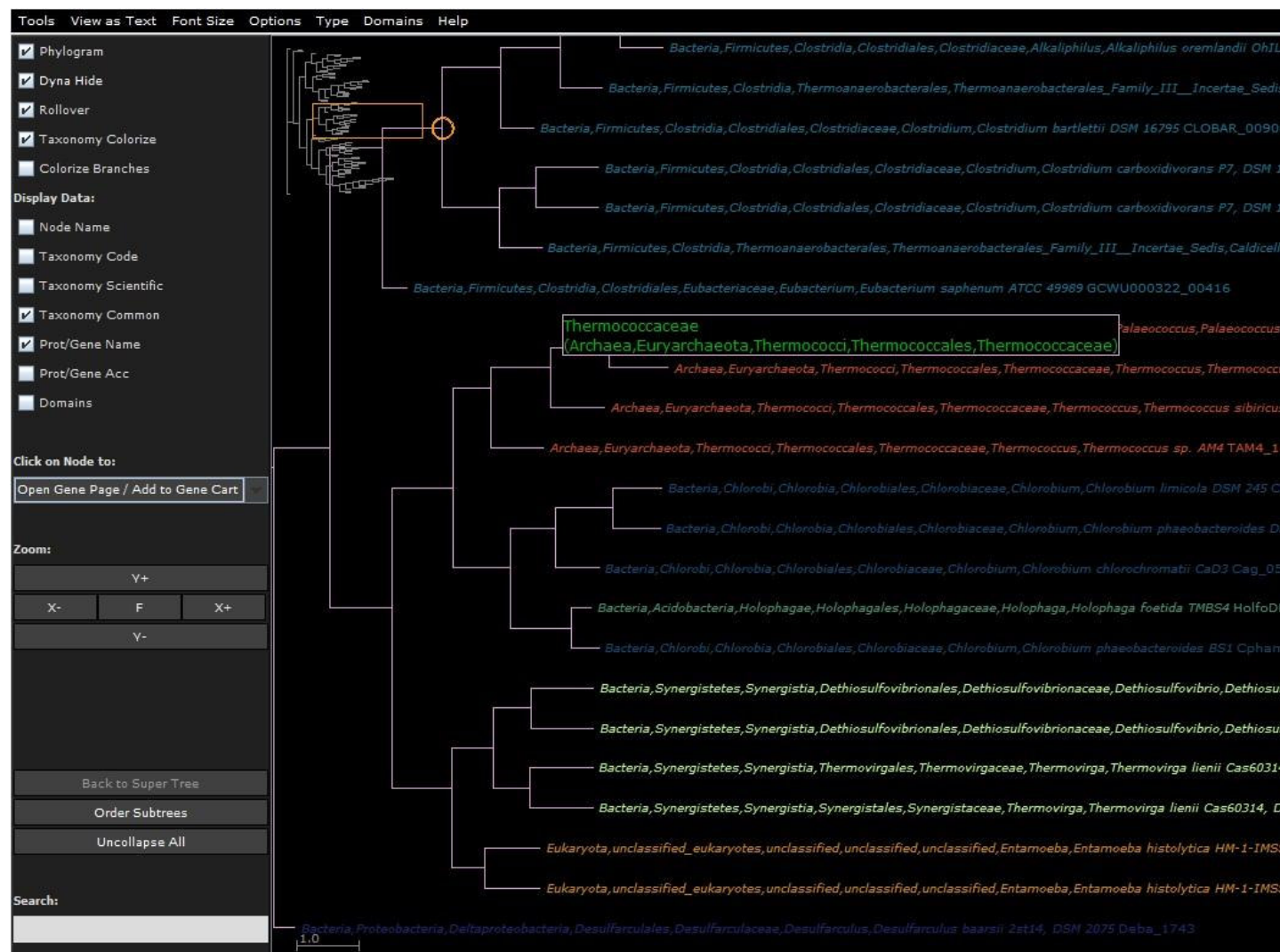


Figure 15 Tool tip

Linking to IMG

Each node in the Archaeopterix applet has a context menu which can be used to link to a page in IMG. In the current version of the applet, that link is renamed to either “Open Gene Page” or “Open Genome Page” for the leaf nodes, depending on whether the tree displays genes or genomes.

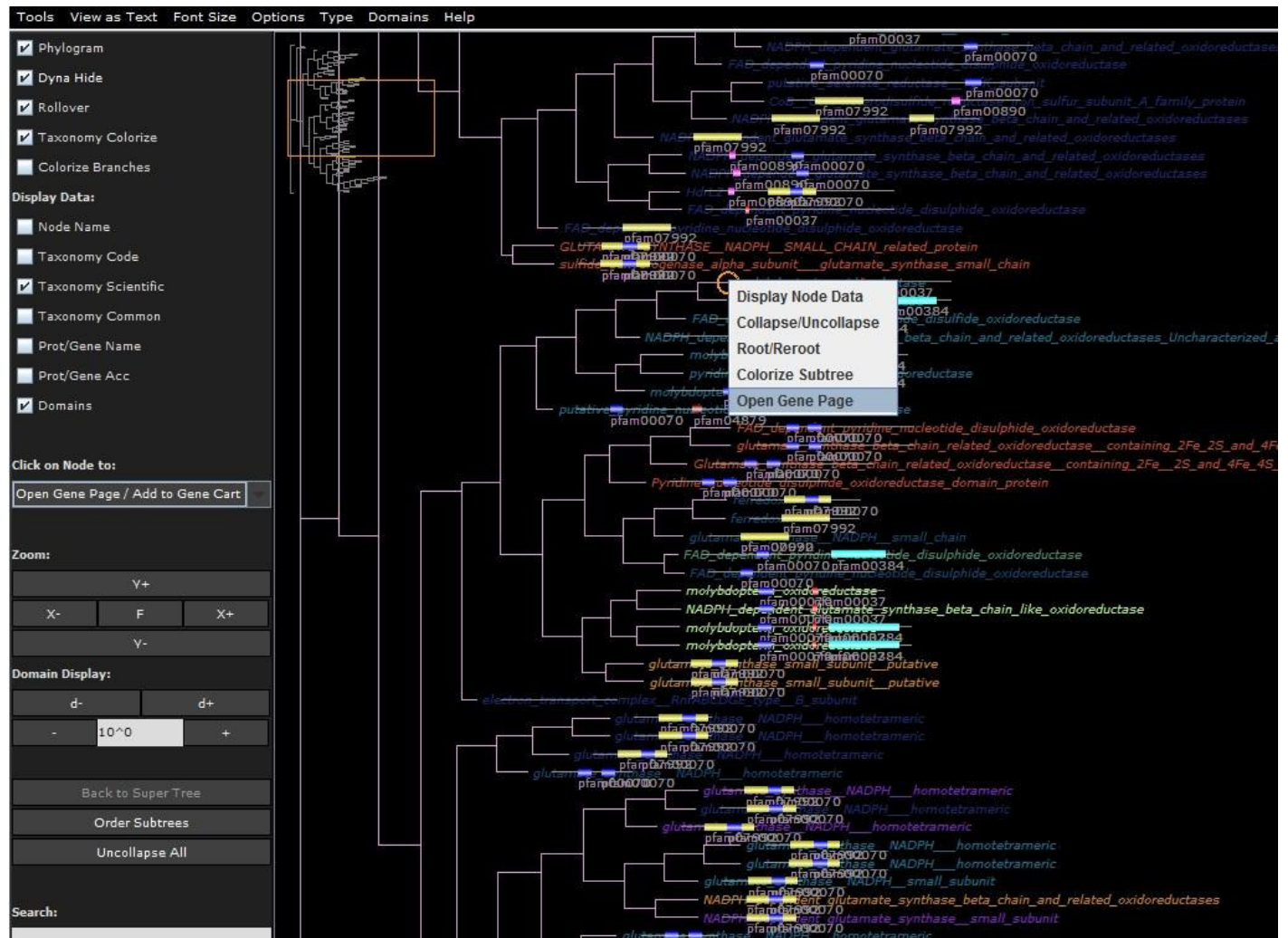


Figure 16 Menu link to IMG

What's New in IMG 3.4

In addition, in ClustalW alignment where the [Archaeopterix applet](#) is used to display domains within genes, the link in the context menu for a parent node, called “Add to Gene Cart” allows the user to add all the genes of child nodes to the gene cart in IMG.

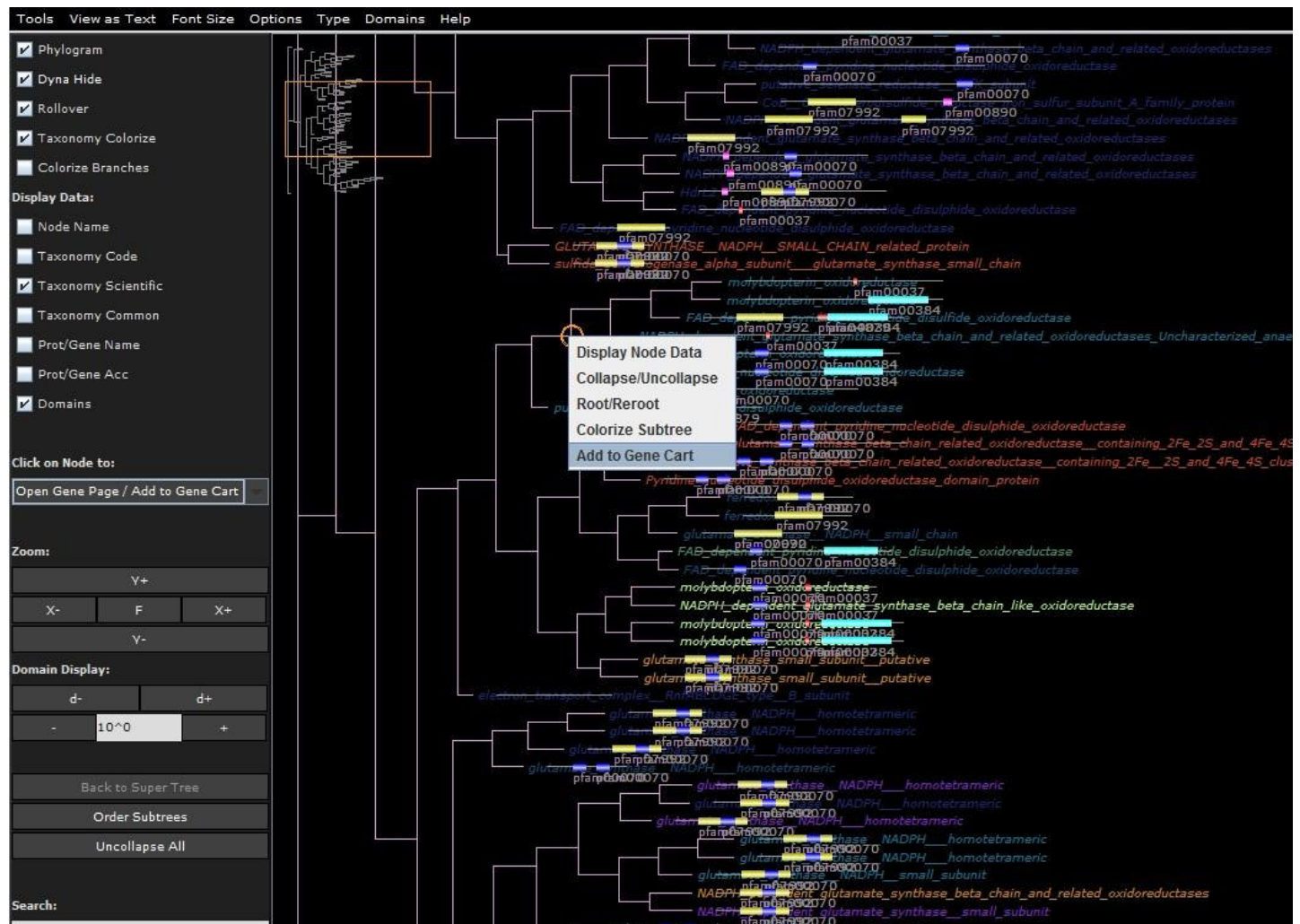


Figure 17 Menu link to add to Gene Cart